

Gencore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model
 Run on: March 15, 2003, 23:25:27 ; Search time 4.44656 Seconds
 (without alignments)
 2525.515 Million cell updates/sec

Title: US-08-978-217-12
 Perfect score: 84
 Sequence: 1 KNSSGWKEEVLOSRN 16

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Xgapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Dlext 7.0

Searched: 501302 seqs, 350932545 residues

Total number of hits satisfying chosen parameters: 1002604

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL:frame_p2n,model -DEV=xlp
 -Q=/cgn2_1/USPTO_spool/US08978217/runat_14032003_141840_13490/app_query.fasta_1.1500
 -DB=Published_Applications_NA -QFMT=fastap -SUFIX=rnbp -MINMATCH=0.1
 -LOOPCH=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
 -TRANS=human40_cci -LIST=45 -DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100
 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pro -NORM=ext -REAPSIZE=0.00 -MTNLEN=0
 -MAXLEN=200000000 -USER=US-08978217 @CGN 1 1 145 @runat 14032003_141840_13490
 -NCPU=6 -ICPU=3 -NO_XLPE=1 -NO_MMAP -LARGEQUERY -NEG_SCORE=0 -WAIT -LONGLOG
 -DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=10 -XGAPEXT=0.5 -RGAPON=6
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DSELEXT=7

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/us07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/us06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/us06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/us07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/PCVUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/us08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/us08_PUBCOMB.seq:*

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10: /cgn2_6/ptodata/2/pubpna/us09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/us10_NEW_PUB.seq:*

12: /cgn2_6/ptodata/2/pubpna/us10_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/us60_NEW_PUB.seq:*

14: /cgn2_6/ptodata/2/pubpna/us60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	84	100.0	451	Sequence 32, Appl Sequence 2290, App Sequence 101, App
2	84	100.0	449	Sequence 32, Appl Sequence 2290, App Sequence 101, App
3	84	100.0	1915	Sequence 32, Appl Sequence 2290, App Sequence 101, App
4	84	100.0	1915	Sequence 32, Appl Sequence 2290, App Sequence 101, App

RESULT 1
 US-09-998-598-32
 ; Sequence 32, Application US/09998598
 ; Patent No. US20020150922A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Chenault, Ruth A.
 ; APPLICANT: Meagher, Madeleine Joy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
 ; FILE REFERENCE: 210121_561
 ; CURRENT APPLICATION NUMBER: US/09/998,598
 ; CURRENT FILING DATE: 2001-11-16
 ; NUMBER OF SEQ ID NOS: 2606
 ; SOFTWARE: Corixa Invention Disclosure Database
 ; SEQ ID NO 32
 ; LENGTH: 451
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-998-598-32

ALIGNMENTS

Alignment Scores:
 Pred. No.: 3.73e-06
 Score: 84.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 Length: 451
 Matches: 16
 Conservative: 0
 Mismatches: 0
 Indels: 0

DB: 10 Gaps: 0

US-08-978-217-12 (1-16) x US-09-998-598-32 (1-451)

QY 1 LysAsnSerSerglyTrpIysGluGluGluValLeuGlnSerArgAsn 16

Db 170 AAAACTCAAGCGCTGGAGAGGGTCTCCAGAGTCGGAC 217

RESULT 2

US-09-998-598-2290/C

; Sequence 2290, Application US/09998598

; Patent No. US20020150522A1

; GENERAL INFORMATION:

; APPLICANT: Stolk, John A.

; APPLICANT: Xu, Jiangchun

; APPLICANT: Chenault, Ruth A.

; APPLICANT: Meagher, Madeleine Joy

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER

; FILE REFERENCE: 210121.561

; CURRENT APPLICATION NUMBER: US/09/998, 598

; CURRENT FILING DATE: 2001-11-16

; NUMBER OF SEQ ID NOS: 2606

; SOFTWARE: Corixa Invention Disclosure Database

; SEQ ID NO 2290

; LENGTH: 499

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-998-598-2290

Alignment Scores:

Pred. No.: 4.21e-06 Length: 499

Score: 84.00 Matches: 16

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

Db: 10 Gaps: 0

US-08-978-217-12 (1-16) x US-09-998-598-2290 (1-499)

QY 1 LysAsnSerSerglyTrpIysGluGluGluValLeuGlnSerArgAsn 16

Db 95 AAAACTCAAGCGCTGGAGAGGGTCTCCAGAGTCGGAC 48

RESULT 3

US-09-964-824A-101

; Sequence 101, Application US/09964824A

; Patent No. US2002010231A1

; GENERAL INFORMATION:

; APPLICANT: Horrigan, Stephen

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu

; FILE REFERENCE: 689290-73

; CURRENT APPLICATION NUMBER: US/09/964, 824A

; CURRENT FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: US/60/236, 033

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US/60/236, 032

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US/60/236, 028

; PRIOR FILING DATE: 2000-09-28

; NUMBER OF SEQ ID NOS: 583

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 101

; LENGTH: 1915

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-964-824A-101

Alignment Scores:

Pred. No.: 2.07e-05 Length: 1915

Score: 84.00 Matches: 16

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

Db: 10 Gaps: 0

US-08-978-217-12 (1-16) x US-09-964-824A-563 (1-1915)

QY 1 LysAsnSerSerglyTrpIysGluGluGluValLeuGlnSerArgAsn 16

Db 1185 AAAACTCAAGCGCTGGAGAGGGTCTCCAGAGTCGGAC 1232

RESULT 5

US-09-880-107-3420

; Sequence 3420, Application US/09880107

; Patent No. US20020142981A1

; GENERAL INFORMATION:

; APPLICANT: Horne, Darci T.

; APPLICANT: Vockley, Joseph G.

; APPLICANT: Scherf, Uwe

; APPLICANT: Gene Logic, Inc.

; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

; FILE REFERENCE: 44911-5028-WO

; CURRENT APPLICATION NUMBER: US/09/880,107

; CURRENT FILING DATE: 2001-05-14

; PRIOR APPLICATION NUMBER: US 60/211,379

; PRIOR FILING DATE: 2000-06-14

; PRIOR APPLICATION NUMBER: US 60/237,054

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 3950

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3420

; LENGTH: 1915

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE: 0

Alignment Scores:

Pred. No.: 2.07e-05 Length: 1915

Score: 84.00 Matches: 16

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 10 Gap: 0

US-08-978-217-12 (1-16) x US-09-964-824A-101 (1-1915)

QY 1 LysAsnSerSerglyTrpIysGluGluGluValLeuGlnSerArgAsn 16

Db 1185 AAAACTCAAGCGCTGGAGAGGGTCTCCAGAGTCGGAC 1232

RESULT 4

US-09-964-824A-563

; Sequence 563, Application US/09964824A

; Patent No. US2002012531A1

; GENERAL INFORMATION:

; APPLICANT: Horrigan, Stephen

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu

; FILE REFERENCE: 689290-73

; CURRENT APPLICATION NUMBER: US/09/964, 824A

; PRIOR APPLICATION NUMBER: US/60/236, 033

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US/60/236, 032

; PRIOR FILING DATE: 2000-09-28

; NUMBER OF SEQ ID NOS: 583

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 563

; LENGTH: 1915

; TYPE: DNA

; ORGANISM: Homo sapiens

Alignment Scores:

Pred. No.: 2.07e-05 Length: 1915

Score: 84.00 Matches: 16

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

Db: 10 Gaps: 0

US-08-978-217-12 (1-16) x US-09-964-824A-563 (1-1915)

QY 1 LysAsnSerSerglyTrpIysGluGluGluValLeuGlnSerArgAsn 16

Db 1185 AAAACTCAAGCGCTGGAGAGGGTCTCCAGAGTCGGAC 1232

; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U73843
; US-09-880-107-3420

Alignment Scores: 2.07e-05 Length: 1915
; Pred. No.: 84.00 Matches: 16
; Score: 100.0% Conservative: 0
; Percent Similarity: 100.0% Mismatches: 0
; Best Local Similarity: 100.0% Indels: 0
; Query Match: 100.0% Gaps: 0
; DB: 10

US-08-978-217-12 (1-16) x US-09-880-107-3420 (1-1915)

QY 1 LysAsnSerSerGlyTrpLysGluGluValLeuGlnSerArgasn 16
; Db 1185 AAAACTCAAGGGCTGGAAGGAGGAGGTCTCAGACTGGAC 1232

RESULT 6

US-09-967-768A-192

; Sequence 192, Application US/09967768A
; Patent No. US2002015087A1

GENERAL INFORMATION:

; APPLICANT: Augustus, Meena

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu

; TITLE OF INVENTION: SatB

; FILE REFERENCE: 659290-72

; CURRENT APPLICATION NUMBER: US/09/967,768A

; CURRENT FILING DATE: 2001-09-28

; PRIOR APPLICATION NUMBER: US/60/236,109

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US/60/236,034

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US/60/236,111

PRIOR FILING DATE: 2000-09-28

NUMBER OF SEQ ID NOS: 325

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 192

LENGTH: 1915

TYPE: DNA

ORGANISM: Homo sapiens

US-09-967-768A-192

Alignment Scores:

Pred. No.: 2.07e-05 Length: 1915
; Score: 84.00 Matches: 16
; Percent Similarity: 100.0% Conservative: 0
; Best Local Similarity: 100.0% Mismatches: 0
; Query Match: 100.0% Indels: 0
; DB: 9

US-09-922-217-105

QY 1 LysAsnSerSerGlyTrpLysGluGluValLeuGlnSerArgasn 16
; Db 1187 AAAACTCAAGGGCTGGAAGGAGGAGGTCTCAGACTGGAC 1234

RESULT 8

US-08-978-217-12 (1-16) x US-10-025-380-1105 (1-1917)

QY 1 LysAsnSerSerGlyTrpLysGluGluValLeuGlnSerArgasn 16
; Db 1187 AAAACTCAAGGGCTGGAAGGAGGAGGTCTCAGACTGGAC 1234

Alignment Scores:

Pred. No.: 2.07e-05 Length: 1917
; Score: 84.00 Matches: 16
; Percent Similarity: 100.0% Conservative: 0
; Best Local Similarity: 100.0% Mismatches: 0
; Query Match: 100.0% Indels: 0
; DB: 9

US-08-978-217-12 (1-16) x US-10-025-380-1105 (1-1917)

QY 1 LysAsnSerSerGlyTrpLysGluGluValLeuGlnSerArgasn 16
; Db 1185 AAAACTCAAGGGCTGGAAGGAGGAGGTCTCAGACTGGAC 1232

RESULT 7

US-10-025-380-1105

; Sequence 1105, Application US/10025380
; Publication No. US20020182191A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Lodes, Michael J.

; APPLICANT: Secrist, Heather

; APPLICANT: Benson, Darin R.

; APPLICANT: Meagher, Madeleine Joy

; APPLICANT: Stolk, John A.

; APPLICANT: Wang, Tongrong

; APPLICANT: Jiang, Yugu

; APPLICANT: Smith, Carole Lynn

; APPLICANT: King, Gordon E.

; APPLICANT: Wang, Aijun

; APPLICANT: Clapper, Jonathan D.

; APPLICANT: Stolk, John A.

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

; FILE REFERENCE: 210121-471C13

; CURRENT APPLICATION NUMBER: US/09/922,217

; CURRENT FILING DATE: 2001-08-03

; NUMBER OF SEQ ID NOS: 1124

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 1105

; LENGTH: 1917

TYPE: DNA

ORGANISM: Homo sapiens

US-09-922-217-1105

Alignment Scores:

Pred. No.: 2.07e-05 Length: 1917
; Score: 84.00 Matches: 16
; Percent Similarity: 100.0% Conservative: 0
; Best Local Similarity: 100.0% Mismatches: 0
; Query Match: 100.0% Indels: 0
; DB: 10

US-08-978-217-12 (1-16) x US-09-922-217-1105 (1-1917)

QY 1 LysAsnSerSerGlyTrpLysGluGluValLeuGlnSerArgasn 16
; Wang, Aijun
; Clapper, Jonathan D.

; APPLICANT: Wang, Tongrong

; APPLICANT: Jiang, Yugu

; APPLICANT: Smith, Carole L.

; APPLICANT: King, Gordon E.

; APPLICANT: Clapper, Jonathan D.

Db 1187 AAAACTCAAGCGCTGGAGGGAGGTTCTCCAGAGTCGGAAC 1234

RESULT 9

US-09-925-301-207

; Sequence 207, Application US/09925301

; Patent No. US2002052308A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA106

; CURRENT APPLICATION NUMBER: US/09/925,301

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05882

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 1694

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO: 207

; LENGTH: 1996

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-301-207

Alignment Scores:

Pred. No.: 2.17e-05

Score: 84.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 10

Length: 1996

Matches: 16

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-08-978-217-12 (1-16) x US-09-925-301-207 (1-1996)

Qy 1 LysAsnSerSerGlyTrpLySgluGluValLeuGlnSerArg 16

Db 1206 AAAACTCAAGCGCTGGAGGGAGGTTCTCCAGTCGGAAC 1253

RESULT 10

; Sequence 40, Application US/09986480

; Publication No. US20030027999A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 143 Human Secreted Proteins

; FILE REFERENCE: PSS00P1

; CURRENT APPLICATION NUMBER: US/09/986,480

; CURRENT FILING DATE: 2001-11-08

; PRIOR APPLICATION NUMBER: PCT/US00/12788

; PRIOR FILING DATE: 2000-05-11

; PRIOR APPLICATION NUMBER: US 60/134,068

; PRIOR FILING DATE: 1999-05-13

; NUMBER OF SEQ ID NOS: 456

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO: 40

; LENGTH: 1681

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE: SITE

; NAME/KEY: SITE

; LOCATION: (6)

; OTHER INFORMATION: n equals a,t,g, or c

; LOCATION: (50)

; OTHER INFORMATION: n equals a,t,g, or c

; US-09-986-480-40

Alignment Scores:

Pred. No.: 0.82

Score: 57.00

Percent Similarity: 81.25%

Best Local Similarity: 62.50%

Query Match: 67.85%

Db: 405 GAAATGACTCAGGTTGGAGTCAGGAAAGCTTCAGTCAGAAGT

RESULT 11

US-08-978-217-12 (1-16) x US-09-986-480-40 (1-1681)

Qy 1 LysAsnSerSerGlyTrpLySgluGluValLeuGlnSerArg 16

; Sequence 678, Application US/09933797

; Patent No. US20020155119A1

; GENERAL INFORMATION:

; APPLICANT: Robert A. Sikes et al.

; TITLE OF INVENTION: Isolation and Use of Fetal Urogenital

; FILE REFERENCE: 9901-007-999

; CURRENT APPLICATION NUMBER: US/09/933,797

; CURRENT FILING DATE: 2001-08-22

; PRIOR APPLICATION NUMBER: US/09/482,933

; PRIOR FILING DATE: 2000-01-14

; PRIOR APPLICATION NUMBER: PCT/US99/10746

; PRIOR FILING DATE: 1999-05/14

; PRIOR APPLICATION NUMBER: 60/085,383

; PRIOR FILING DATE: 1998-05-14

; NUMBER OF SEQ ID NOS: 811

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO: 678

; LENGTH: 174

; TYPE: DNA

; ORGANISM: Murine

; US-09-933-797-678

Alignment Scores:

Pred. No.: 2.01

Score: 48.00

Percent Similarity: 73.33%

Best Local Similarity: 53.33%

Query Match: 57.14%

DB: 9

Length: 174

Matches: 8

Conservative: 3

Mismatches: 4

Indels: 0

Gaps: 0

US-08-978-217-12 (1-16) x US-09-933-797-678 (1-174)

Qy 1 LysAsnSerSerGlyTrpLySgluGluValLeuGlnSerArg 15

Db 78 AAGCACTTAGGAGGCTGGAGCAGGAGGATTCTGCAGGTCGA 34

RESULT 12

; Sequence 4493, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harmer, Jeff

; APPLICANT: Krcps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; TITLE OF INVENTION: SAME, AND METHODS OF USE

; FILE REFERENCE: SCRIPI300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-06-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO: 4493

; LENGTH: 1571

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

; US-09-938-842A-4493

Alignment Scores:

Pred. No.: 60.2

Score: 46.00

Percent Similarity: 56.25%

Best Local Similarity: 50.00%

Query Match: 54.76%

Db: 9

Length: 1571

Matches: 8

Conservative: 1

Mismatches: 7

Indels: 0

Gaps: 0

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/901,106
 FILING DATE: 10-Jul-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/07/920,281C
 FILING DATE: 13-AUG-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Murphy Jr., Gerald M.
 REGISTRATION NUMBER: 28,977
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-341-1200
 TELEFAX: 703-241-2848
 TELEX: 248345

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1517 base pairs
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA (Genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 TYPE: nucleic acid
 ORIGINAL SOURCE:
 ORGANISM: Semliki Forest Virus
 FEATURE:
 NAME/KEY: -
 LOCATION: 1..11517
 OTHER INFORMATION: /label= genome
 /note= "Semliki Forest Virus complete nucleotide
 sequence, presented as a cloned DNA sequence; see
 Figure 5."
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 87..7379
 OTHER INFORMATION: /product= "SFV polyprotein"

FEATURE:
 NAME/KEY: CDS
 LOCATION: 7421..11179
 OTHER INFORMATION: /product= "SFV polyprotein"
 /SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-901-106-1

Alignment Scores:

Pred. No.: 133

Score: 46.00

Percent Similarity: 83.33%

Best Local Similarity: 66.67%

Query Match: 54.76%

Db: 9

Length: 3060

Matches: 8

Conservative: 2

Mismatches: 2

Indels: 0

Gaps: 0

Alignment Scores:

Pred. No.: 638

Score: 46.00

Percent Similarity: 85.71%

Best Local Similarity: 50.00%

Query Match: 54.76%

Db: 10

Length: 11517

Matches: 7

Conservative: 5

Mismatches: 2

Indels: 0

Gaps: 0

Alignment Scores:

Pred. No.: 3

Score: 4018

Percent Similarity: 56.25%

Best Local Similarity: 50.00%

Query Match: 54.76%

Db: 716

Length: 16

Matches: 16

Conservative: 16

Mismatches: 16

Indels: 16

Gaps: 16

Alignment Scores:

Pred. No.: 675

Score: 4018

Percent Similarity: 56.25%

Best Local Similarity: 50.00%

Query Match: 54.76%

Db: 716

Length: 716

Matches: 716

Conservative: 716

Mismatches: 716

Indels: 716

Gaps: 716

Alignment Scores:

Pred. No.: 1477

Score: 4018

Percent Similarity: 56.25%

Best Local Similarity: 50.00%

Query Match: 54.76%

Db: 1512

Length: 1512

Matches: 1512

Conservative: 1512

Mismatches: 1512

Indels: 1512

Gaps: 1512

Alignment Scores:

Pred. No.: 1477

Score: 4018

Percent Similarity: 56.25%

Best Local Similarity: 50.00%

Query Match: 54.76%

Db: 1512

Length: 1512

Matches: 1512

Conservative: 1512

Mismatches: 1512

Indels: 1512

Gaps: 1512

Alignment Scores:

Pred. No.: 1477

Score: 4018

Percent Similarity: 56.25%

Best Local Similarity: 50.00%

Query Match: 54.76%

Db: 1512

Length: 1512

Matches: 1512

Conservative: 1512

Mismatches: 1512

Indels: 1512

Gaps: 1512

Alignment Scores:

Pred. No.: 1477

Score: 4018

Percent Similarity: 56.25%

Best Local Similarity: 50.00%

Query Match: 54.76%

Db: 1512

Length: 1512

Matches: 1512

Conservative: 1512

Mismatches: 1512

Indels: 1512

Gaps: 1512

Alignment Scores:

Pred. No.: 1477

Score: 4018

Percent Similarity: 56.25%

Best Local Similarity: 50.00%

Query Match: 54.76%

Db: 1512

Length: 1512

Matches: 1512

Conservative: 1512

Mismatches: 1512

Indels: 1512

Gaps: 1512

Alignment Scores:

Pred. No.: 1477

Score: 4018

Percent Similarity: 56.25%

Best Local Similarity: 50.00%

Query Match: 54.76%

Db: 1512

Length: 1512

Matches: 1512

Conservative: 1512

Mismatches: 1512

Indels: 1512

Gaps: 1512

Alignment Scores:

Pred. No.: 1477

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Matches: 1512

Conservative: 1512

Mismatches: 151

